## AMENDMENTS TO THE CLAIMS

1. (Original) A method for the fermentative production of at least one sulfur-containing fine chemical, which comprises the following steps:

a) fermentation of a coryneform bacteria culture producing the desired sulfur-containing fine chemical, the coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with O-acetylhomoserine sulfhydrolase (metY) activity;

b) concentration of the sulfur-containing fine chemical in the medium or in the bacterial cells, and

c) isolation of the sulfur-containing fine chemical.

2. (Original) A method as claimed in claim 1, wherein the sulfur-containing fine chemical comprises L-methionine.

3. (Currently amended) A method as claimed in claim 1 ~~either of the preceding claims~~, wherein the heterologous metY-encoding nucleotide sequence is less than 100% homologous to the metY-encoding sequence from Corynebacterium glutamicum ATCC 13032.

4. (Original) A method as claimed in claim 3, wherein the metY-encoding sequence is derived from any of the following organisms:

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|---|---|
| Corynebacterium diphteriae | ATCC 14779 |
| Mycobacterium tuberculosis CDC1551 | ATCC 25584 |
| Clostridium acetobutylicum | ATCC 824 |
| Bacillus halodurans | ATCC21591 |
| Bacillus stearothermophilus | ATCC 12980 |
| Chlorobium tepidum | ATCC 49652 |
| Synechococcus sp. | ATCC27104 |
| Emericella nidulans | ATCC 36104 |
| Bacteroides fragilis | ATCC 25285 |
| Lactococcus lactis | ATCC 7962 |

| | |
|---|---|
| Bordetella bronchiseptica | ATCC 19395 |
| Pseudomonas aeruginosa | ATCC 17933 |
| Nitrosomonas europaea | ATCC 19718 |
| Sinorhizobium meliloti | ATCC 4399 |
| Thermotoga maritima | ATCC 43589 |
| Streptococcus mutans | ATCC 25175 |
| Burkholderia cepacia | ATCC 25416 |
| Deinococcus radiodurans | ATCC 13939 |
| Rhodobacter capsulatus | ATCC 11166 |
| Pasteurella multocida | ATCC 6530 |
| Clostridium difficile | ATCC 9689 |
| Campylobacter jejuni | ATCC 33560 |
| Streptococcus pneumoniae | ATCC 6308 |
| Saccharomyces cerevisiae | ATCC 2704 |
| Kluyveromyces lactis | ATCC 8585 |
| Candida albicans | ATCC 10231 |
| Schizosaccharomyces pombe | ATCC 24969 |

5. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein the metY-encoding sequence comprises a coding sequence according to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51 and 53 or a nucleotide sequence homologous thereto which codes for a protein with metY activity.

6. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein the metY-encoding sequence codes for a protein with metY activity, said protein comprising an amino acid sequence according to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52 and 54 or an amino acid sequence homologous thereto which represents a protein with metY activity.

7. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein the coding metY sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

8. (Original) A method as claimed in claim 7, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metY sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metY sequence has been integrated into the bacteria chromosome is used.

9. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein the coding metY sequence is overexpressed.

10. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of the desired sulfur-containing fine chemical has been amplified or mutated such that its activity is not influenced by metabolic metabolites.

11. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein bacteria are fermented in which at least one metabolic pathway, which reduces the production of the desired sulfur-containing fine chemical, is at least partially switched off.

12. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among

a) the gene lysC, which encodes an aspartate kinase,

b) the glyceraldehyde-3-phosphate dehydrogenase-encoding gene gap,

c) the 3-phosphoglycerate kinase-encoding gene pgk,

d) the pyruvate carboxylase-encoding gene pyc,

e) the triose phosphate isomerase-encoding gene tpi,

f) the homoserine O-acetyltransferase-encoding gene metA,

g) the cystathionine gamma-synthase-encoding gene metB,

h) the cystathionine gamma-lyase-encoding gene metC,

i) serine hydroxymethyltransferase-encoding gene glyA,

j) the methylene tetrahydrofolate reductase-encoding gene metF,

k) the vitamin B12-dependent methionine synthase-encoding gene metH,

l) the phophoserine aminotransferase-encoding gene serC,

m) the phosphoserine phosphatase-encoding gene serB,

n) the serine acetyltransferase-encoding gene cysE, and

o) the gene hom, which encodes a homoserine dehydrogenase,

is overexpressed or mutated in such a way that the activity of the corresponding proteins is influenced by metabolic metabolites to a smaller extent, if at all, compared to nonmutated proteins.

13. (Currently amended) A method as claimed in claim 1 ~~any of the preceding claims~~, wherein coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among

a) the homoserine kinase-encoding gene thrB,

b) the threonine dehydratase-encoding gene ilvA,

c) the threonine synthase-encoding gene thrC,

d) the meso-diaminopimelate D-dehydrogenase-encoding gene ddh,

e) the phosphoenolpyruvate carboxykinase-encoding gene pck,

f) the glucose-6-phosphate 6-isomerase-encoding gene pgi,

g) the pyruvate oxidase-encoding gene poxB,

h) the dihydrodipicolinate synthase-encoding gene dapA,

i) the dihydrodipicolinate reductase-encoding gene dapB; and

j) the diaminopicolinate decarboxylase-encoding gene,

is attenuated by changing the rate of expression or by introducing a specific mutation.

14. (Currently amended) A method as claimed in claim 1 ~~one or more of the preceding claims~~, wherein microorganisms of the species Corynebacterium glutamicum are used.

15. (Original) A method for producing an L-methionine-containing animal feed additive from fermentation broths, which comprises the following steps:

a) culturing and fermentation of an L-methionine-producing microorganism in a fermentation medium;

b) removal of water from the L-methionine-containing fermentation broth;

c) removal of from 0 to 100% by weight of the biomass formed during fermentation; and

d) drying of the fermentation broth obtained according to b) and/or c), in order to obtain the animal feed additive in the desired powder or granule form.

16. (Currently amended) A method as claimed in claim 15, wherein the microorganisms ~~according to the definition in any of claims 1 to 14 are used~~ are coryneform bacteria expressing at least one nucleotide sequence which codes for a protein with metY activity.